

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 01:27:49 ; Search time 544.842 Seconds  
(without alignments)  
10849.659 Million cell updates/sec

Title: US-09-856-979-7

Perfect score: 365  
Sequence: 1 tcagccagacaaatgggggc.....tccatcaagccgtcgatg 365

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

- 1: em\_estba:\*
- 2: em\_esthum:\*
- 3: em\_estim:\*
- 4: em\_estmu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_est3:\*
- 13: gb\_est4:\*
- 14: gb\_est5:\*
- 15: em\_estfun:\*
- 16: em\_estom:\*
- 17: gb\_gss:\*
- 18: em\_gss\_hum:\*
- 19: em\_gss\_inv:\*
- 20: em\_gss\_pln:\*
- 21: em\_gss\_vrt:\*
- 22: em\_gss\_fun:\*
- 23: em\_gss\_mam:\*
- 24: em\_gss\_mus:\*
- 25: em\_gss\_other:\*
- 26: em\_gss\_pro:\*
- 27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	11.2	764	9 AL565922	AL565922
2	39	10.7	391	14 C74001	C74001 C74001 Rice
3	37.8	10.4	571	10 BE044167	BE044167 ho39e01.x
4	37.8	10.4	960	9 AL528127	AL528127 AL528127
5	37.8	10.4	966	9 AL528272	AL528272 AL528272
6	37.4	10.2	969	17 AZ551127	AZ551127 ENTNDLITR

7	37.2	10.2	777	9	AL553672	AL553672
8	37	10.1	574	9	AU029306	AU029306
9	37	10.1	841	9	AL582386	AL582386
c 10	36.8	10.1	429	14	W44754	W44754 zc78c03.r1
c 11	36.6	10.0	476	17	BH018696	BH018696 LI922k.d
c 12	36.6	10.0	493	17	L2025Y	AL354102 Leishmani
13	36.6	10.0	916	9	AL564785	AL564785
14	36.4	10.0	1165	14	BM904449	BM904449 AGENCOURT
15	36.2	9.9	893	9	AL527787	AL527787
16	36.2	9.9	958	17	CNS044HE	AL274091 Tetradon
17	36.2	9.9	1028	9	AL545506	AL545506
18	35.8	9.8	957	9	AL574284	AL574284
19	35.8	9.8	995	9	AL562554	AL562554
c 20	35.6	9.8	994	13	BM459131	BM459131 AGENCOURT
21	35.6	9.8	1169	17	AG142795	AG142795 Pan trogl
22	35.6	9.8	1327	12	BE914468	BE914468
23	35.4	9.7	519	17	BH233534	BH233534 1006174C0
24	35.4	9.7	912	9	AL563783	AL563783
25	35	9.6	430	12	BF733514	BF733514 RC6-AN006
26	35	9.6	452	12	BF733516	BF733516 RC6-AN006
c 27	35	9.6	484	14	BM697674	BM697674 UI-E-DX0-
c 28	35	9.6	561	13	BM507336	BM507336 i127e07.Y
c 29	35	9.6	570	13	BI717755	BI717755 1031021G1
c 30	35	9.6	585	14	BM830316	BM830316 K-EST0103
c 31	35	9.6	586	14	BM769817	BM769817 K-EST0053
c 32	35	9.6	639	10	BE263421	BE263421 601190678
c 33	35	9.6	644	10	AW391273	AW391273 QVO-ST021
c 34	35	9.6	657	14	BM769366	BM769366 K-EST0052
c 35	35	9.6	670	14	BM726988	BM726988 UI-E-EJ0-
c 36	35	9.6	671	13	BI222337	BI222337 602939713
c 37	35	9.6	706	14	BM718786	BM718786 UI-E-E01-
c 38	35	9.6	716	14	BM769332	BM769332 K-EST0052
c 39	35	9.6	787	12	BF348220	BF348220 60202136
c 40	35	9.6	794	12	BG402941	BG402941 602418744
c 41	35	9.6	802	12	BF862180	BF862180 963032A08
c 42	35	9.6	832	13	BM006545	BM006545 603615511
c 43	35	9.6	863	13	BI766676	BI766676 603057447
c 44	35	9.6	864	12	BE993685	BE993685 601436486
c 45	35	9.6	883	14	BQ670113	BQ670113 AGENCOURT

#### ALIGNMENTS

RESULT 1  
AL565922  
LOCUS AL565922 LTI\_FL013\_FBrnl Homo sapiens cDNA clone CS0DF009YG24 3  
DEFINITION prime, mRNA sequence.  
ACCESSION AL565922  
VERSION AL565922.1 GI:12917777  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 764)  
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
FEATURES  
1. 764  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0DF009YG24"  
/clone\_lib="LTI\_FL013\_FBrnl"  
/dev\_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"  
/lab\_host="DH10B"



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AL528127
LOCUS       AL528127 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC025YB12 3
DEFINITION prime, mRNA sequence.
ACCESSION  AL528127
VERSION     AL528127.1 GI:12791620
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 960)
AUTHORS     Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES             Location/Qualifiers
     source           1..966
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="LTI_NFL003_NBC3"
                     /sex="male"
                     /tissue_type="neuroblastoma cells"
                     /lab_host="DH10B"
                     /note="organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed
                     by Life Technologies. Contact : Feng Liang Life
                     Technologies, a division of Invitrogen 9800 Medical Center
                     Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
                     8371 Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"

BASE COUNT   243 a 247 c 285 g 179 t 12 others
ORIGIN
Query Match      10.4%; Score 37.8; DB 9; Length 966;
Best Local Similarity 53.1%; Pred. No. 2.2;
Matches 78; Conservative 1; Mismatches 68; Indels 0; Gaps 0;

QY 172 GTGGACGCGTGAGGTGCTTTCGCCATGACCGCTCTGTGGTTGTTCAGTCACTTGGCGACG 231
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 662 GCGATCGAGAGAGGTGGAGGTGAGGTGACTGGCCATGGCTGTATTCTGGACTTGTGGCAG 721

QY 232 CTTCGACCGTGACTACCTGCCACATTCGCCCGCGCTGCCGCGCCCTACAAAAGCCAC 291
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 722 CYGGGACAGGGTCTGCTCTGCGTTATTATACAGGAGGAGCTGCAGCTGCAACTGCCTC 781

QY 292 ACACGACCGCGGCCACGATACCCAT 318
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 782 ATAGGACCGGGCAGCAGCGGCGCCCTT 808

RESULT 6
AL551127/c
LOCUS       AL551127 Entamoeba histolytica Sheared DNA Entamoeba histolytica
DEFINITION genomic, DNA sequence.
ACCESSION  AL551127
VERSION     AL551127.1 GI:11176428
SOURCE      GSS.
ORGANISM    Entamoeba histolytica.
            Eukaryota; Entamoebidae; Entamoeba.
REFERENCE   1 (bases 1 to 969)
AUTHORS     Loftus, B., Van Aken, S. and Fraser, C.
TITLE       Determination of clone end sequences from Entamoeba histolytica
            HMI:IMSS sheared DNA library
JOURNAL     Unpublished (2000)
COMMENT     Contact: Brendan J Loftus
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0208
            Fax: 301 838 3543
            Email: b.loftus@tigr.org
            Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
            DNA library
            Seq primer: MJ3-Reverse
            Class: shotgun
            high quality sequence start: 325
            high quality sequence stop: 569.
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